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SUMMARIES

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ALIGNMENTS

peptide SEQ ID NO 41.

RESULT 1
AAM48538
ID AAM48538;
XX AC AAM48538;
XX 20-MAR-2002 (first entry)
XX 20-MAR-2002 (first entry)
XX Anti-inflammatory peptide SEQ
XX Anti-inflammatory; antiasthmati
KW Antiinflammatory; antiasthmati
KW Antiinflammator; antiarthritic;
KW immunosuppressive; dermatologi
KW cytokine; NFkappaB; IkappaB ki
KW cytokine; NFkappaB; IkappaB ki
KW cytokine; NFkappaB; IkappaB ki
KW antiallergic; membrane translo
KW cytokine; NFkappaB; IkappaB ki
KW antiallergic; multiple
costeoporosis; Altheimer's dise
KW osteoporosis; Altheimer's dise
KW autoimmune disorder; multiple
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KW cytokine; NFkappaB ki
KW autoimmune disorder; multiple
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KW cytokine; NFkappaB;
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KW autoimmune disorder; multiple
costeoporosis; Altheimer's dise
KW cytokine; NFkappaB; LicappaB ki
KW autoimmatory; compound
PT May MJ, Ghosh S, Findeis MA,
XX (PRAE-) PRAECIS PHARM INC.
PA (PRA Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.

2001WO-US014346.

2000US-0201261P. 2000US-00643260.

Findeis MA, Phillips K;

Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappal activation, and for treating asthma, lung inflammation, psoriasis. kappaB

English

The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The

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RESULT 2
AAM48570
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antiatherosclerotic, virucide and antiallergic activity. The compounds

cact as selective inhibitors of cytokine-mediated NFkappaB activation by

blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding

cdomain that results in inhibition of IKKbeta kinase activation and

subsequent decreased phosphorylation of IKKbeta kinase activation and

cancer, psoriasis, rheumatory disorders, e.g. asthma, lung inflammation or

cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory

bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as

chappaB activation and

crancer, psoriasis, inflammatory esponses, sutoimmune diseases, such as

crancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory

bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as

cransplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;

crancer sutorions; and ataxia telangiectasia. The compounds are also

useful for treating pro-inflammatory responses such as allergies,

curticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,

crancer sutorions, and arthritis

crancer sutorions, and arthritis

crancer sutorions, and arthritis
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Best Local
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                                                Novel antiin fused to NEN activation,
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                                                                                                                       WPI;
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22-AUG-2000;
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                                                                                                                       2002-121889/16
                                               antiinflammatory compound
to NEMO binding sequence,
ation, and for treating as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                  compound comprising membrane translocation domain sequence, useful for blocking nuclear factor kappa sating asthma, lung inflammation, psoriasis.
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Claim

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RESULT 3
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ID ADA61814;
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AC ADA61814;
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NEMO bind
KW NEMO bind
KW Antiarthr
KW antiarthr
KW antiarthr
KW gene ther
KW psoriasis
KW inflammat
KW systemic
KW systemic
KW systemic
KW alzheimer
KW necrosis
XX
OS Unidentif
XX
PN US2003054
XX
PD 20-MAY-20
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PF 02-MAY-20
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PF 02-MAY-20
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PI May MJ,
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DR WPI; 2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunosuppressive, dermatological, neuropacnic, antibacterial, cc antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IkKbeta kinase activation and subsequent decreased phosphorylation of IkKbeta kinase activation and cancer, psoriasis, rheumatory disorders, e.g. asthma, lung inflammation or bowel disease, sepsis, vasculitis, bursitis, autoimmune diseases such as clupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis, cransplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; cural infections; and ataxia telangiectasia. The compounds are also curticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, curburn, aging and arthritis
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                         NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta; antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic; antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic; antiarthritic; osteopathic; antibacterial; immunosuppressive; dermatological; neuroprotective; cytostatic; nootropic; virucid gene therapy; anti-inflammatory; inflammatory disorder; asthma; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; sepsis; vasculitis; autoimmune disesystemic lupus erythematosus; multiple sclerosis; cancer; osteo Alzheimer's disease; viral infection; NF-kappa B essential modulator.
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SH S.
DEIS M A.
LIPS K.
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                                      Findeis MA,
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Pred. No. 1.4e+06;
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                                        Phillips
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                                        <u>ი</u>
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l modulator;
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RESULT 4
ADA61846
ID ADA6
XX ADA6
XX ADA6
XX ADA6
XX NFAI
XX NEMC
KW NEMC
KW NEMC
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cancer, c
sequence.
                         asthma, cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy; anti-inflammatory; inf psoriasis; rheumatoid arthritis; ost inflammatory bowel disease; sepsis; systemic lupus erythematosus; multip Alzheimer's disease; viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic antiarthritic; osteopathic; antibacterial; immunosuppressive dermatological; neuroprotective; cytostatic; nootropic; virus gene therapy; anti-inflammatory; inflammatory disorder; asthribasis; rheumatoid arthritis; osteoarthritis;
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                                                                                                   flammatory compound comprising membrane translocation domain to binding sequence, useful for blocking nuclear factor kappal and for treating asthma, lung inflammation, psoriasis.
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residues, fur antiinflammat antirheumation

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on relates to an antiinflammatory compound (especially 448645), comprising a membrane translocation domain (AAM, AAM48646-AAM48651) which comprises from 6-15 amino acid used to a NEMO binding sequence (AAM48525-AAM48619). The story compounds have antiasthmatic, cytostatic, antipsoric, antiarthritic, osteopathic, antibacterial,

(AAM48525-AAM48619). The cic, cytostatic, antipsoriatic

(AAM48620-

The invention AAM48628-AAM4

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Query Match
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Matches 6
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                                     New compasthma, cancer,
                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                     NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta; antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic; antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic; antiinflammatory; antipacterial; immunosuppressive; dermatological; neuroprotective; cytostatic; nootropic; virucide; gene therapy; anti-inflammatory; inflammatory disorder; asthma; psoriasis; rheumatoid arthritis; osteoarthritis; psoriasis; rheumatoid arthritis; osteoarthritis; autoimmune disease; systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis; Alzheimer's disease; viral infection; NF-kappa B essential modulator; necrosis factor kappa B essential modulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NFkB
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antiallergic;
cytokine; NFk
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The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, nootropic,
                                                                                                                                                                                                                                                                                                                                                                            WPI;
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activation, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
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                                      antiinflammatory compound comprising to NEMO binding sequence, useful for ation, and for treating asthma, lung:
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The invention relates to an antiinflammatory AAM48628-AAM48645), comprising a membrane tra AMM48627 or AAM48646-AAM48651) which comprise

.ammatory compound brane translocation 6-:

6-1

(especially n domain (AAM48620) 15 amino acid

asthma,

psor

iasis,

for diagnosing or treating inflammatory disorders, e.g. asis, rheumatoid arthritis, inflammatory bowel disease

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compound

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RESULT 9
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                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta; antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic; antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic; antiarthritic; osteopathic; antibacterial; immunosuppressive; dermatological; neuroprotective; cytostatic; nootropic; viruciogene therapy; anti-inflammatory; inflammatory disorder; asthmatisoriasis; rheumatoid arthritis; osteoarthritis;
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                                                                                                                                                                                                            (MAYM/)
(GHOS/)
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                                                                                 6541/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               al modulator (NEMO) binding peptide #51.
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                                                                                                                                                                                                                                                                                                                                                2000US-0201261P.
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Pred. No. 1.4e+06;
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ple sclerosis; cancer; on; NF-kappa B essential
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                                                                                                                               Hannig G;
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l modulator;
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Matches
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antiarthritic; osteopathic; antibacterial; immunosup
dermatological; neuroprotective; cytostatic; nootrop
gene therapy; anti-inflammatory; inflammatory disord
psoriasis; rheumatoid arthritis; osteoarthritis;
inflammatory bowel disease; sepsis; vasculitis; auto
systemic lupus erythematosus; multiple sclerosis; ca
Alzheimer's disease; viral infection; NF-kappa B ess
necrosis factor kappa B essential modulator
                                                                                    asthma, cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes an anti-inflammatory compound comprising (I). The compound is useful for diagnosing or treating inflammatory disorders, such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g. systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis, Alzheimer's disease or viral infection. This is the amino acid sequence of an anti-iflammatory peptide that binds to, and down-regulates, necrosis factor kappa B (NFkB) essential modulator (NEMO).
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                                                                                    or treating inf larthritis, in translocation
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pry disorder; asthma;
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s; cancer; osteoporosis;
B essential modulator;
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ry bowel disease
nd a NEMO binding
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Alzheimer
of an ant
The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620 AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriation antirheumatic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                                                                                                                                                                                                                                                                                                                                    Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappal activation, and for treating asthma, lung inflammation, psoriasis.
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22-AUG-2000;
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                                                                                                                      Novel antiinflammatory compound fused to NEMO binding sequence, activation, and for treating as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunosuppressive; dermatological; neuroprotective; antiallergic; membrane translocation domain; NEMO bi cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; carheumatoid arthritis; osteoarthritis; inflammatory kautoimmune disorder; multiple sclerosis; transplant osteoporosis; Alzheimer's disease; atherosclerosis;
The invention relates to an antiinflammatory compound (especial AAM48628-AAM48645), comprising a membrane translocation domain AMM48627 or AAM48646-AAM48651) which comprises from 6-15 amino residues, fused to a NEMO binding sequence (AAM48525-AAM48619). antiinflammatory compounds have antiasthmatic, cytostatic, anti
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Novel antiinfl fused to NEMO activation, an

NO binding sequence, usefund for treating asthma,

flammatory compound comprising membrane translocation domain obinding sequence, useful for blocking nuclear factor kappa and for treating asthma, lung inflammation, psoriasis.

kappaB

2002-121889/16.

Claim

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Page

62; 88pp;

English

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RESULT 14
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Novel antiinflammatory compound fused to NEMO binding sequence, activation, and for treating ast

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y membrane transloc r blocking nuclear inflammation, pso

translocation d nuclear factor ion, psoriasis.

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                                                                                                                                                                                                                                                                                                                                                                                                          New compound for diagnosing or treating inflammatory disorders, e.g. asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or cancer, comprises a membrane translocation domain and a NEMO binding sequence.
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1: /cgn2_6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

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10: /cgn2_6/ptodata/1/pubpaa/US09A PUBCOMB.pep:*

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13: /cgn2_6/ptodata/1/pubpaa/US09 NEW PUB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10A PUBCOMB.pep:*

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16: /cgn2_6/ptodata/1/pubpaa/US10C PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10 NEW PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US60_NEW PUB.pep:*

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US-09-847-946A-72
US-09-847-946A-72
US-09-847-946A-75
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ALIGNMENTS

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RESULT 1

US-09-847-946A-41

; Sequence 41, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-08-22-
NUMBER: OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 41
. LENGTH: 6
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; TYPE: PRT
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                                                                                                                                                                                                                                                                     APPLICANT: Finder.,
APPLICANT: Phillips, Kathry...
APPLICANT: Hannig, Gerhard
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY CO
TITE REFERENCE: PPI-119
TTE REFERENCE: PPI-119
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TITLE OF INVENTION: ANTI-INFLAMMATORY CO
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,94
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
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APPLICANT: Ghosh, Sankar
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APPLICANT: Ghosh, Sankar
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ORGANISM: Artificial
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Phillips, Kathryn
Hannig, Gerhard
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Findeis, Mark A
Phillips, Kathryn
Hannig, Gerhard
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RESULT 5
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US-09-847-946A-78
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OTHER INFORMATION:
US-09-847-946A-70
                                                                                                                                                               APPLICANT: Ghosh, Sankar

APPLICANT: Findeis, Mark A

APPLICANT: Phillips, Kathryn

APPLICANT: Hannig, Gerhard

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUN

FILE REFERENCE: PPI-119

CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: 60/201,261

PRIOR FILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 160

SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNTIONE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
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LENGTH: 8
TYPE: PRT
ORGANISM: 1
FEATURE:
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GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Artificial 9
FEATURE:
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Findeis, Mark A
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Wannig, Gerhard
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US-09-847-946A-
                                                                                                        APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COFILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847, 94
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201, 261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643, 260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
                                                                                   SOFTWARE:
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                            Sequence 72, Appublication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Best I
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APPLICANT: May, Mic
APPLICANT: Ghosh,
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GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh. Carling
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PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
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APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
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                                         TYPE: PRT ORGANISM:
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TYPE: PRT
ORGANISM: Artificial
OTHER INFORMATION: OTHER INFORMATION:
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Phillips, Kathryn
Hannig, Gerhard
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               Sequence: NEMO binding
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; OTHER INFORMATION:
US-09-847-946A-75
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CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: 60/201,261

PRIOR FILING DATE: 2000-05-02

PRIOR APPLICATION NUMBER: 09/643,260

PRIOR FILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 160

NUMBER OF SEQ ID NOS: 160
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US-09-847-
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PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02-
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: May, Mic
APPLICANT: Ghosh,
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Publication No
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CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
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APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS
FILE REFERENCE: PPI-119
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                         TYPE: PRT ORGANISM:
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Ghosh,
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Ghosh, Saunce
Findeis, Mark A
Phillips, Kathryn
Phillips, Kathryn
Thomig, Gerhard
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ENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
NCE: PPI-119
NCE: PPI-119
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vo. US20030054999A1
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Artificial Sequence: NEMO binding
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No. 1e+06;
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APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 71
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US-09-847-946A-76
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US-09-847-946A-
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US-09-847-946A-
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           SOFTWARE:
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APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
                                                 PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02-
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
                                          NUMBER OF
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LENGTH: 10
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ORGANISM: Artificial
FEATURE:
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Pred. No. 1e+
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RESULT 12
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OTHER INFORMATION:
US-09-847-946A-74
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-847-946A-68
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Matches 6
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SEQ ID NO 68
LENGTH: 11
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Publication No. US20030203467A1
GENERAL INFORMATION:
APPLICANT: Gualfetti, Peter
APPLICANT: Mitchinson, Colin
APPLICANT: Phillips, Jay Ian
TITLE OF INVENTION: Novel Variant EGIII-Like
TITLE OF INVENTION: Compositions
                                              CURRENT APPLICATION NUMBER: US/10/441,625
CURRENT FILING DATE: 2003-05-19
NUMBER OF SEQ ID NOS: .64
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH. 226
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TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
10-441-625-1
                                                                                                                        FILE REFERENCE: GC631
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TYPE: PR
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Ghosh, Sankar
: Findeis, Mark A
: Phillips, Kathryn
''annig, Gerhard
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RESULT 14
US-10-441-626-17
; Sequence 17, Applicat
; Publication No. US200
; GENERAL INFORMATION:
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US-09-815-242-5090
; Sequence 5090, Application US/09815242;
Perent No. US20020061569A1
APPLICANT: Oblisen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICATION NUMBER: 60/261,91,078
PRIOR APPLICATION NUMBER: 60/266,848
PRIOR APPLICATION NUMBER: 60/264,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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; TYPE: PRT
; ORGANISM: Gliocladium
US-10-441-626-17
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APPLICANT: Mitchinson, Colin
APPLICANT: Mitchinson, Colin
APPLICANT: Phillips, Jay Ian
TITLE OF INVENTION: No. US20030186418A1el Va
TITLE OF INVENTION: Compositions
FILE REFERENCE: GC631
CURRENT APPLICATION NUMBER: US/10/441,626
CURRENT FILING DATE: 2003-05-19
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 236
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; ORGANISM: Pseudomonas aeruginosa
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Q9i389 pseudomonas
Q825el streptomyce
Q9acr5 streptomyce
Q9ar5 streptomyce
Q9ixk8 homo sapien
Q7ygu8 sphenodon p
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Q8g659 bifidobacte
Q86ks0 dictyosteli
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ALIGNMENTS

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                                                                                                             E SEQUENCE FROM N.A.

P SEQUENCE FROM N.A.

MEDLINE=22067395; PubMed=12073090;

A Goedegebuur F., Fowler T., Phillips J., van der Kley P.,

A Goedegebuur F., Fowler T., Phillips J., van der Kley P.,

A van Solingen P., Dankmeyer L., Power S.D.;

"Cloning and relational lanalysis of 15 novel fungal endoglucanases

T from family 12 glycosyl hydrolase.";

Curr. Genet. 41:89-98(2002).

R EMBL; AF435065; AAM77708.1; -..

R GO; GO:0008810; F:cellullase activity; IEA.

GO; GO:0000272; P:polysaccharide catabolism; IEA.

R GO; GO:0000272; P:polysaccharide catabolism; IEA.

R InterPro; IPR008985; ConA like lec gl.

R InterPro; IPR002594; Glyco hydro 12; 1.

R ProDom; PD004316; Glyco hydro 12; 1.

R ProDom; PD004316; Glyco hydro 12; 1.

SEQUENCE 236 AA; 26024 MW; C3D8A7E33F0C41D8 CRC64;
                                                        Query Match
Best Local
Matches
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Q8NJY9;
01-OCT-2002
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                             Endoglucanase.

CEL12C.

Bionectria ochroleuca (Gliocladium roseum).

Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Bionectriaceae; Bionectria.

NCBI_TaxID=29856;
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RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley N.
RA Pridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflect
RT to the human gastrointestinal tract.";
Proc. Natl. Acad. Sci. U.S.A. 99:14427-14427(2002).
NR EMBL; AE014701; AAN24605.1; -.
RGO; GO:0016491; F:oxidoreductase activity; IEA.
R GO; GO:0006118; P:electron transport; IEA.
R GO; GO:0006118; P:electron transport; IEA.
R Ffam; PF00970; FAD_binding_6; 1.
Complete proteome.
SEQUENCE 274 An
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Best Local
Matches
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Q96KS0;

Q96ACC

                     Baumgart C.;
Submitted (MAR-2003) to the EMB!
EMBL; AC115612; AAO50929.1; -.
GO; GO:0003824; F:catalytic act;
GO; GO:0008152; P:metabolism; I!
InterPro; IPR000581; ILVD_EDD_f:
InterPro; IPR006970; PT.
Pfam; PF04886; PT; 1.
PROSITE; PS00886; ILVD_EDD_1; 1
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01-MAR-2003 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
Probable dihydroorotate d
PYRK OR BL0790.
Bifidobacterium longum.
Bacteria; Actinobacteria;
Bifidobacteriaceae; Bifid
NCBI_TaxID=216816;
[1]
SEQUENCE FROM N.A.
STRAIN=NCC 2705;
MEDLINE=22294977; PubMed=
Schell M.A., Karmirantzou
                                                                                                                                                                                                                                                             SEQUENCE FROSTRAIN=AX4;
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Q8G659;
01-MAR-2003
01-MAR-2003
01-OCT-2003
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l Similarity 83.3%;
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)bacteria; Actinobacteridae
!ae; Bifidobacterium.
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23, Last sequence update
25, Last annotation update
dehydrogenase electron (
                                                                                                                                                                                activity;
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ed. No. 2.6e+02;
Mismatches 0;
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RESULT
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Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. A
EMBL; AL59179
Hypothetical
SEQUENCE 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Pro
Rhizobiaceae;
NCBI_TaxID=38
SEQUENCE FROM N.A.

STRAIN=1021;

MEDLINE=213,96507; PubMed=11481430;

Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Dreano S., Gloux Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021.";
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Q92K30
01-DEC-
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01-DEC-2001 (TrEMBLrel. 19, Last sequence used)
01-MAR-2002 (TrEMBLrel. 20, Last annotation Hypothetical protein R02283.
R02283 OR SMC01671.
Rhizobium meliloti (Sinorhizobium meliloti)
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37 AA; 48372 MW; 950E0B3DA963CE78
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(TrEMBLrel. 19, Last sequence up)
(TrEMBLrel. 20, Last annotation
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1; Mismatc
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                                                                                        Drosophila melanogaster (Fruit fly).

Drosophila melanogaster (Fruit fly).

C Exkaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

C Ephydroidea; Drosophilidae; Drosophila.

C Roptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

C Ephydroidea; Drosophilidae; Drosophila.

X NCBI_TaxID=7227;

X NCBI_TaxID=7227;

N [1]

P SEQUENCE FROM N.A.

STRAIN=Berkeley;

A Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

STRAIN=Berkeley;

A Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.

A George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,

A Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.

A Pàtel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.

Celniker S.;

A Patell S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.

Celniker S.;

A Celniker S.;

Celniker S.;

A Colo004197; F:cysteine-type endopeptidase activity; IEA.

GO; GO:000618; P:proteolysis and peptidolysis; IEA.

GO; GO:000618; P:proteolysis and peptidolysis; IEA.

GO; GO:000618; P:proteolysis and peptidolysis; IEA.

InterPro; IPR000172; GMC_oxred_C.

InterPro; IPR000172; GMC_oxred_C.

R Pfam; PF05199; GMC_oxred_C; 1.

Pfam; PF05199; GMC_oxred_N; 1.

Pfam; PF05199; GMC_oxred_N; 1.

PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.

SEQUENCE 581 AA; 63475 MW; A2F13BEBC25E496D CRC64;
                                               Query Naest Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Naest Lo
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004009; F:ATP-binding cassette (#
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR003439; ABC transporter.
InterPro; IPR003873; AMP-bind.
Pfam; PF00501; AMP-binding; 1.
PROSITE; PS00455; AMP-BINDING; 1.
Ligase; Complete proteome.
SEQUENCE 548 AA; 59383 MW; 659A68C546
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Q8MSH3;
Q8MSH3;
01-OCT-2002 (TrEM
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NINAG OR CG6728.
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RA MARDINE-2019-006; PunMed=1073112;
RA Adams M.D. Celniker S.E., Holt R.A., Byans C.A., Godayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Byans C.A., Godayne J.D.,
RA Adams M.D., Celniker S.E., Richards S. Ashburner M., Henderson S.N.,
RA Button G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y. H.C., Blazef R.G., Change M., Pfeiffer B.D.,
RA MAR K.H., Doyle C., Baxer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Blashlys R.
RA Belson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshlyov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokeein P., Erottler P.,
RA Durbin K.J., David C.S., Perraz C., Ferrica S., Pfeischmann H.,
RA Durbin K.J., David C.S., Perraz C., Ferrica S., Pfeischmann H.,
RA Durbin K.J., David C.S., Perraz C., Ferrica S., Fleischmann H.,
RA Pfeier C., Gabrielan A.R., Garg N.S., Gelbart M.M., Fleischmann H.,
RA Harris N.L., Harvey D., Helmann T.J., Hernandes J.R., Houck J.,
RA Harris N.L., Harvey D., Helmann T.J., Keil M.-H., Ibegwam C.,
RA Jalai M., Kalush P., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
RA Harris M.K., Houston K.A., Howland T.J., Keil M.-H., Ibegwam C.,
RA Jalai M., Kalush P., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitkey A.A., Li J., Li Z., Liang Y., Lin X.,
RA Mang J. P., Lei Y., Levitkey A.A., Li J., Li Z., Liang Y., Lin X.,
RA Malazzolo M., Pitteman G.S., Pan S., Nurphy L., Muzny D. M., Nelson D.L.,
RA Malazzolo M.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Malazzolo M.R., Nelson S.I., Singson M., Skupski M.P., Smith T.,
RA Spier B., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier B., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier B., Spradling A.C., Stapleton M., Skupski M.P., Smith H.O.,
RA Mann M., Woy M., Murphy B., Murphy J., Muzny D., M., Nelson D.L.,
RA Mall M., Woy M., Murphy B., Murphy J., Muzny D., Man S., Yao Q.A.,
RA Mall M., Sh
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SEQUENCE FROM N.A.
STRAIN=Berkeley;
MEDLINE=20196006;
Adams M.D., Celnik,
Amanatides P.G., S.
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NCBI_TaxID=72
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melanogaster (Fruit fly).
Metazoa; Arthropoda; Hexapoda; Insecta; Pterygol
Endopterygota; Diptera; Brachycera; Muscomorpha;
• Prosophilidae; Drosophila.
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                 larity
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Score 37; DB 5; Le
Pred. No. 5.7e+02;
l; Mismatches 0;
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RESULT
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D 086712;

C 086712;

T 01-NOV-1998 (TrEMBLrel. 08, Created)

T 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

T 01-NOV-1998 (TrEMBLrel. 24, Last annotation update)

T 01-UN-2003 (TrEMBLrel. 24, Last annotation update)

Hypothetical protein SC06530.

S SC06530 OR SC5C7.15:

S Streptomyces coelicolor.

C Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

STREPTOMYCINEAE; Streptomycetaceae; Streptomyces.

C Streptomycineae; Streptomycetaceae; Streptomyces.

(1)

SEQUENCE FROM N.A.

C STRAIN=A3(2) / M145;

MEDLINE=21996410; PubMed=12000953;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

A Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins

A Cromin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth

A Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.

A Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

A Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor

A Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.

Hopwood D.A.;

T Complete genome sequence of the model actinomycete Streptomyces

T coelicolor A3(2).";

C SHELL; AL939128; CAA20627.1;

N RIFT; T35222; T35222.

W Hypothetical protein; Complete proteome.

SEQUENCE 610 AA; 67368 MW; 052CEA90DB589021 CRC64;
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Matches
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TTU
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Q91389;
01-MAR-2001
01-MAR-2001
01-OCT-2003
SEQUENCE FROM N.A.

STRAIN=ATCC 15692 / PAO1;

MEDLINE=20437337; PubMed=10984043;

MEDLINE=20437337; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagro Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R. Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                 Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=287;
[1]
SEQUENCE FROM N.A.
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KDPD OR PA1636.
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parkhill J.,
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ser H.,
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P SEQUENCE FROM N.A.

C STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;

X MEDLINE=21477403; PubMed=11572948;

X MEDLINE=21477403; PubMed=11572948;

X MEDLINE=21477403; PubMed=11572948;

A Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,

A Nikuchi H., Ishikawa J., Hanamoto A., Takahashi C.,

A Kikuchi H., Shiba T., Sakaki Y., Hattori M.;

"Genome sequence of an industrial microorganism Streptomyces

avermitilis: deducing the ability of producing secondary

metabolites.";

Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
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Best Loc
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SEQUENCE FF
STRAIN=MA-4
MEDLINE=226
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n-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
22608306; PubMed=12692562;
, Ishikawa J., Hanamoto A., Shinose M., Kikuch
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tinobacteria; Actinobacteridae; Actinomycetales; eae; Streptomycetaceae; Streptomyces.
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Pred. No. 8.5e+02;
L; Mismatches 0;
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                QBIXK8
QBIXK8;
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01-MAR-2003 (TrEMBLrel. 2:
01-MAR-2003 (TrEMBLrel. 2
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"Complete genome sequence and compar
microorganism Streptomyces avermitil
Nat. Biotechnol. 21:526-531(2003).
EMBL; AP005050; BAC75228.1; -.
Hypothetical protein; Complete prote
SEQUENCE 173 AA; 18912 MW; 22B26
                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome s
coelicolor A3(2)."
Nature 417:141-147
EMBL; AL590464; CP
GO; GO:0046821; C:
Hypothetical prote
SEQUENCE 205 AA;
Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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SCP1.253.
Streptomyces
Plasmid SCP1.
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Q9ACR5;
01-JUN-
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Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser Harper D., Bateman A., Brown S., Chandra G., Chen C.W., C Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., H Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., C Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter Seeger K., Saunders D., Sharp S., Squares R., Squares S., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Act: Streptomycineae; Streptomycetaceae; Streptomyce; NCBI_TaxID=1902; [1]
SEQUENCE FROM N.A.
STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hopwood D.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                    nplete genome sequence of the model actinomycelicolor A3(2).";
ure 417:141-147(2002).
L; AL590464; CAC36779.1; -.
GO:0046821; C:extrachromosomal DNA; IEA.
othetical protein; Plasmid; Complete proteome
UENCE 205 AA; 23051 MW; 6602396CFF93F2D9 (
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Similarity 83.3%;
5; Conservative
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                 Chordata;
Primates;
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23, Last sequence 23, Last announce protein BC017
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Last sequence up
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Pred. No. 2.4e+02;
); Mismatches 1
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ermitilis.";
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                   Craniata; V Catarrhini;
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22B26C7D2
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                                                                        sequence update) annotation update 3C017335.
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s S., Taylor
Parkhill J.,
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RESULT 14
Q919K8
ID Q919K
AC Q919K
AC Q919K
DT 01-DE
DT 01-DE
DT 01-DE
CUNOC
GN CUNOC
OS Cules
OC Virus
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Q7YGU8
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Best Local
Matches
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=Florida1997;
MEDLINE=21488685; Pu
Afonso C.L., Tulman
Becnel J.J., Rock D.
"Genome Sequence of
"Genome Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rest J.S., Ast J.C., Austin C.C., Wad Hay J.M., Mindell D.P.; "Molecular systematics of primary rep mitochondrial genome."; Mol. Phylogenet. Evol. 0:0-0(2003). EMBL; AF534390; AAP42708.1; -. Mitochondrion. SEQUENCE 228 AA; 25903 MW; AC5244
                                                                                                                                                                                                                                                                             Q919K8;
Q919K8;
01-DEC-2001 (
01-DEC-2001 (
01-DEC-2001 (
CUN068 hypoth
CUN068.
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Q7YGU8;
01-OCT-2003
01-OCT-2003
01-OCT-2003
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Sphenodon punctatus (Hatteria) (Tuatara).
Mitochondrion.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Sphenodontia; Sphenodontidae; Sphenodon.
NCBI_TaxID=8508;
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SEQUENCE FROM N.A.
TISSUE=Brain;
Strausberg R.;
Strausberg R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
EMBL; BC040173; AAH40173.1; -.
Hypothetical protein.
SEQUENCE 227 AA; 25487 MW; F11A71EA57062A05 CRC64;
                                                                                                                                                                                                                   Culex nigripalpus baculovirus. Viruses; dsDNA viruses, no RNA NCBI_TaxID=130556;
      EQUENCE
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                                   ...man B.R., Lu Z., Balinsky C
., Rock D.L., Kutish G.F.;
quence of a Baculovi
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3 (TrEMBLrel. 25, Last sequence update)
3 (TrEMBLrel. 25, Last annotation update)
oxidase subunit II.
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                                                                    a Baculovirus Pathogenic
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annotation update)
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3.1e+02;
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                                                                                                            C.A.,
                                                                  for Culex nigripalpus
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RESULT 15
Q8BIT9
ID Q8BIT
AC Q8BIT
DT 01-MADT 01-MADT 01-MADT 01-MADT 01-OC
DE Mitoc
GN 28104
OS MUS 0
OC EUKAX
OC MAMMAD
OX NCBI-
RN [1]
RN [1]
RR SEQUE
RC STRAJ
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Search completed: Job time: 41 secs
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Matches
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C QBBIT9;
C QBBIT9;
C O1-MAR-2003 (TrEMBLrel. 23, Created)
T 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
T 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
T 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
T 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Micochondrial ribosomal protein L41 homolog.

N 2810443J12RIK.

S Mus musculus (Mouse).
E whatyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos (Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae (NCBI_TAXID=10090;

[1]
PSEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=NOD; TISSUE=Thymus;
The FANTOM Consortium,
The FANTOM Consortium,
A the RIKEN Genome Exploration Research Group Phase I & II Teather Fanty of the mouse transcriptome based on functional annotation for the mouse transcr
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Afonso C.L., Tulman E.R., Lu Z., Balinsky C.A.,
Becnel J.J., Rock D.L., Kutish G.F.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ da
EMBL; AF403738; AAK94146.1; -.
Hypothetical protein.
SEQUENCE 242 AA; 27222 MW; 6014967531110E52
                                                                                                                                                                                                                                                                                                                                                  Match
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Query Match 92.5%; Score 37; DB 2; Length 885; Best Local Similarity 83.3%; Pred. No. 1.5e+02; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	: C83441 reliminary type: DNA 1-885 <sto> erences: GB:AE004 tal source: strai</sto>	m, X.Q.; Erwin, A.L.; Brody, L.L.; Coult M.V. , 2000 enome sequence of Ps	ESULT 2 83441 wo-component;Species: Ps;Date: 15-Se	Qy 1 ADWSWA 6	Query Match 92.5%; Score 37; DB 2; Length 610; Best Local Similarity 83.3%; Pred. No. 1e+02; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-610 <see> A;Cross-references: EMBL:AL031515; PIDN:CAA20627.1; GSPDB:GN00070; SCOEDB:SC5C7.15 A;Experimental source: strain A3(2) C;Genetics: A;Gene: SCOEDB:SC5C7.15</see>	RESULT 1 T35222 hypothetical protein SC5C7.15 SC5C7.15 - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence revision 05-Nov-1999 #text_change 05-Nov-1999 C;Accession: T35222 R;Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, September 1998 A;Reference number: Z21572 A:Accession: T15222

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RESULT 4
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TonB-dependent receptor [import C;Species: Caulobacter crescent C;Date: 20-Apr-2001 #sequence_C;Accession: E87304
R;Nierman, W.C.; Feldblyum, T.B.; Laub, M.T.; DeBoy, R.T.;
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hypothetical protein T5K18.170 -
C; Species: Arabidopsis thaliana (
C; Date: 23-Apr-1999 #sequence_rev
C; Accession: T05822
R; Bevan, M.; Van Der Schueren, J.
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                                                                                                                                                                                                                      n, J.; Ermolaeva, M.; Whi
Proc. Natl. Acad. Sci. U.
A;Title: Complete Genome
A;Reference number: A8724
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A;Status: preliminary
A;Molecule type: DNA
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R;Stover, C.K.;
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Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa A;Reference number: A82950; MUID:20437337; PMID:10984043

A;Accession: B83241

A;Status: preliminary
A;Molecule type: DNA
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Boy, R.T.; Dodson, R.J.; Durkin, A.S.; Gv
.; White, O.; Salzberg, S.L.; Shapiro, L
ci. U.S.A. 98, 4136-4141, 2001
enome Sequence of Caulobacter crescentus
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K.R.; Kas,
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                         Volckaert
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Larbig,
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C;Species:
C;Date: 02
C;Accessio
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A; Molecule type: DNA
A; Residues: 1-1842 <S
A; Cross-references: E
C; Genetics:
A; Note: 1sd1+
C; Superfamily: yeast
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A;Molecule type: DNA
A;Residues: 1-275 <BE
A;Cross-references: F
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C; Date: 21-Ja
C; Accession:
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A;Map position: 4
A;Introns: 103/3; 141/3; 169/1; 206/3
A;Note: T5K18.170
                                                                                                                                R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N., Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: C84922
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A;Molecule type: DNA
A;Residues: 1-617 <STO>
A;Cross-references: GB:AE002093;
C;Genetics:
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N;Alternate
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Cell Biol. 134, S
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rabidopsis thaliana (mouse-ear cress)
eb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C84922
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ant mitosis in fission yeast mutants defective in fatty acid synth
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ltransferase; coenzyme A
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ilarity 66.7%;
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Score 34; DB 2; Li
Pred. No. 9.4e+02;
2; Mismatches 0;
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Pred. No. 3.1e+02
2; Mismatches
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Pred. No. 1.4e+02;
2; Mismatches 0;
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                                 Length 1842;
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mel-13a protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-19;
C;Accession: S65785
R;Tetsu, O.; Kanno, R.; Isono, K.; Taniguchi, M.
Biochim. Biophys. Acta 1305, 109-112, 1996
A;Title: Cloning and characterization of two trantices consisted and characterization of two trantices; preliminary
A;Accession: S65785
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-132 <TET>
A;Cross-references: EMBL:U35309
C;Genetics:
A;Gene: mel-13
C;Superfamily: mouse mel-13a protein
C;Keywords: alternative splicing
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T38781
fatty acid synthase, subunit alpl
C;Species: Schizosaccharomyces por
C;Date: 03-Dec-1999 #sequence_re
C;Accession: T38781
R;Skelton, J.; Churcher, C.M.; B
submitted to the EMBL Data Libra
conserved hypothetical protein X:
C; Species: Xylella fastidiosa
C; Date: 18-Aug-2000 #sequence_re
C; Accession: B82531
R; anonymous, The Xylella fastidio
Nature 406, 151-157, 2000
A; Title: The genome sequence of
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S65785
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A; Accession: T38781
A; Status: preliminary; translated
A; Molecule type: DNA
A; Residues: 1-1842 < SKE>
A; Cross-references: EMBL: Z98762; F
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A;Map position: 1
C;Superfamily: yeast fat
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s: Schizosaccharomyces pombe
03-Dec-1999 #sequence_revision
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plant
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August 1997
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RESULT 12

S58353

CD1b protein - sh

C;Species: Ovis c

C;Date: 14-Jan-19

C;Accession: S583
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A; Note: for a
A; Accession:
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R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
A;Reference number: A59328
A;Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rson, J.D.; Sadow,
Science 273, 1058-
A; Authors: Kaine,
                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-reference
C;Genetics:
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A;Accession: D64316
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     restriction modification enzyme subunit M1 homolog - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2002
C;Accession: D64316
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C; Genetics:
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Ers: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii. ence number: A64300; MUID:96337999; PMID:8688087
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96 #sequence_revision
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80.10%;
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1; Mismatches
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Pred. No. 1.6e+02;
1; Mismatches 0
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                       ammon aries
01-Mar-1996
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RESULT 13
D90470
hypothetical protein cysH [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_chan
C;Accession: D90470
R;She, Q: Singh, R.K.; Confalonieri, F: Zivanovic, Y.; Alli
Jong, I: Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: D90470
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-239 <KUR>
A;Cross-references: GB:AE006641; NID:g13816282; PIDN:AAK4301:
C;Genetics:
A;Gene: CysH
C;Superfamily: 3'-phosphoadenosine 5'-phosphosulfate reductar
conserved hypothetical protein ML1945 [imported] -
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001
C;Accession: D87152
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K
R; Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K
R; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmo
A;Title: Massive gene decay in the leprosy bacillus
A;Reference number: A86909; MUID:21128732; PMID:112
A;Accession: D87152
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-257 <STO>
A;Cross-references: GB:AL450380; NID:g13093601; PID
C;Genetics:
A;Gene: ML1945
C;Superfamily: Mycobacterium tuberculosis hypotheti
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A;Description: The ovine CD1 gene family contains at
A;Reference number: S58353
A;Recession: S58353
A;Accession: S58353
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-232 <FER>
A;Cross-references: EMBL:X90567; NID:g945010; PIDN:CA
C;Superfamily: class I histocompatibility antigen; in
F;115-180/Domain: immunoglobulin homology <IMM>
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PMID:11234002
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goc, H.P.; Redder,
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-276 <WHI>
A;Cross-references: GB:AE002032; G
A;Experimental source: strain R1
C;Genetics:
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B75337

hypothetical protein - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000

C;Accession: B75337

R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dc., M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zale S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodu A;Reference number: A75250; MUID:20036896; PMID:10567266

A;Accession: B75337

A;Accession: B75337
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A;Map po
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0; Mismatches 1;
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T.; Zalewski,
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Virology 193:868-876(1993)
-!- FUNCTION: Removes the
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Saito T., Kawaoka Y., Webster R.G.;
"Phylogenetic analysis of the N8 neuraminidase
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SUBUNIT: Homotetramer.
SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped spike on the surface of the virion.
SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
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Saito T., Kawaoka
"Phylogenetic anal
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Virology 193:868-876(1993).
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SUBUNIT: Homotetramer.
SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped spike on the surface of the virion.
SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
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Neuraminidase
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-!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
-!- SUBUNIT: Homotetramer.
-!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped spike on the surface of the virion.
-!- SIMILARITY: Belongs to family 24 -f
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=93212520; PubMed=8460490;
MEDLINE=93212520; PubMed=8460490;
Saito T., Kawaoka Y., Webster R.G.;
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Viruses; ssRNA negative strand viruses; Orthomyxoviridae;
Influenza A viruses; Influenzavirus A.
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rPro; IPR001860; Gly; PF00064; neur; 1.
om; PD000431; Glycoom; PD000431; Glycoolase;
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Jeneur; 1.
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TY: Belongs to family 34 of glycosyl hydrolases.
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ANCHOR (BY SIMILARITY).
HYPERVARIABLE STALK REGION.
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"Phylogenetic
viruses.";
Virology 193:8
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Pfam; PF00
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I_TaxID=38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chains of the host cell surface proteins and from carbohydrate side envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.

CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.

SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped spike on the surface of the virion.

SIMILARITY: Belonce +> 2-1.
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IMILARITY: Belongs to family 34 of
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Naoka Y., Webster
analysis of the
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ANCHOR (BY SIMILARITY).

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ssRNA negative-strand viruses; Orthomyxoviridae;
a A viruses; Influenzavirus A.
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se (EC 3.2.1.18).
                  virus (strain A/Equine/Jillin/1/89).
NA negative-strand viruses; Orthomyxoviridae;
viruses; Influenzavirus A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Removes the terminal sialic acid from carbohydrate side if the host cell surface proteins and from the viral. Such a reaction prevents self-aggregation and facilitate lity of the virus to and from the site of infection. C ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, ->8)-glycosidic linkages of terminal sialic residues in charides, glycoproteins, glycolipids, colominic acid and
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4; neur; 1.
0431; Glyco_hydro_34;
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waoka Y., Webster R.G.;
c analysis of the N8 neuraminidase gene of influenza A
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Glycoprotein;
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ANCHOR (BY SIMILARITY).
HYPERVARIABLE STALK REGION.
HEAD OF NEURAMINIDASE.
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P SEQUENCE FROM N.A.

X MEDLINE=93212520; PubMed=8460490;

X Saito T., Kawaoka Y., Webster R.G.;

YT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A viruses.";

RL Virology 193:868-876(1993).

CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral cenvelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.

CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in coligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.

CC --- Substrates.

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InterPro; IPR001860; Glyco_Pfam; PF00064; neur; 1.
ProDom; PD000431; Glyco_hycur; 1
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SEQUENCE FROM N.A MEDLINE=93212520; Saito T., Kawaoka
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[_TaxID=38965;
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J860; Gly

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 PubMed=8460490;
Y., Webster R.G.;
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293
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ive-strand viruses; Orthomyxoviridae
Influenzavirus A.
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ANCHOR (BY SIMILARITY).
HYPERVARIABLE STALK REGION.
HEAD OF NEURAMINIDASE.
BY SIMILARITY.
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SEQUENCE FROM
MEDLINE=93212
Saito T., Kaw
"Phylogenetic
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Virology 193:
-!- FUNCTION:
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01-FEB-1995 (
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28-FEB-2003 (
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                                           2520; PubMed=8460490;
waoka Y., Webster R.G
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NA negative-strand viruses; Orthomyxoviridae;
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Pfam; PF00064; neur; 1.
R ProDom; PD000431; G1yco hydro 34
Hydrolase; G1ycosidase; G1ycopro
TRANSMEM 7 38
FT DOMAIN 89 470
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FT ACT SITE 273 273
ACT SITE 275 275
FT CARBOHYD 46 46
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TARBOHYD 293 293
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/S_APIME STANDARD; PRT
/MRJ5_APIME STANDARD; PRT
/MRJ5_APIME STANDARD; PRT
/MRJ5_2;

28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequent
/MRJP5.

Apic mellifera (42, Last annotation
/MRJP5.

Apis mellifera (40neybee).

Eukaryota; Metazoa; Arthropoda; Honeybee).

Eukaryota; Metazoa; Arthropoda; Honeybee).

NCBI_TaxID=7460;

[1]

SEQUENCE FROM N.A.

TISSUE=Head;

MEDLINE=99373663; PubMed=10441680
Albert S., Bhattacharya D., Klaud

"The family of major royal jelly in the family of m
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DLINE=99373663; rumine D., Klaudiny J., bert S., Bhattacharya D., Klaudiny J., bert S., May of major royal jelly proteins and Mol. Evol. 49:290-297(1999).

- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN HE FOUND IN THE ROYAL JELLY WHICH IS THE FOCUMENTAL JELLY DETERMINES THE DEVIOUS THE HIGH RIED FOR THE F
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SUBUNIT: Homotetramer.

SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped spike on the surface of the virion.

SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
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ANCHOR (BY SIMILARITY).
HYPERVARIABLE STALK REGIO:
HEAD OF NEURAMINIDASE.
BY SIMILARITY.
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BY SIMILARITY.
OF N-LINKED (GLCNAC. . .) (PON-LINKED (GLCNAC. . .) (PON-LINKE
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SEQUENCE FROM
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30-MAY-2000
10-OCT-2003
Polygalactur
PGG1.
EMBL; AF0852
InterPro; II
InterPro; II
Pfam; PF0025
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Eukaryota; F
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                                                                                                     between
the Europ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal;
                                                                                                                                                  Ribon A.B., Coelho J.L.C., Barros E.G., Araujo E.F.;
"Cloning and characterization of a gene encoding the
endopolygalacturonase of Penicillium griseoroseum.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
galactosiduronic linkages in pectate and other galacturonans.
-!- SIMILARITY: Belongs to family 28 of glycosyl hydrolases.
                                                                   use by non-profi
modified and this
entities requires
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SUBCELLULAR LOCATION:
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IPR006626; PbH1.
I95; Glyco hydro 28; 1
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                                                           mail to license@isb-sib.ch)
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                                                                   Bioinformatics Institute. There profit institutions as long as this statement is not removed. United a license agreement (See htt.)
                                                                                                     OT entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation - Bioinformatics Institute. There are no restrictions on its
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42,
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42, Last annotation update)
precursor (EC 3.2.1.15) (PG)
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                                                                                                                                                                                                                                                                                   mitosporic Trichocomaceae; Penicillium.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAJOR ROYAL JELLY PROTEIN 5.
N-LINKED (GLCNAC. . .) (POTE
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Mismatches
                        28
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87;
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RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Weltjens I., Vanstreels E., Rieger M., Walsh S.V., Warren T., Whitehead S.,
WA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
WA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
WA Gabel C., Fichs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
WA Gaffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
A Galibert F., Aves S.J., Xiang Z., Hunt C., Mottier S.,
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y [2]
SEQUENCE FROM N.A.
p SEQUENCE FROM N.A.
K MEDLINE=21363051; PubMed=11470243;
K MEDLINE=21363051; Nakamura K., Inoue K MEDLINE=21363051;
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C15-JUL-1998 (Rel. 36, Created)
C16-OCT-2001 (Rel. 40, Last sequence update)
C28-FEB-2003 (Rel. 41, Last annotation update)
Fatty acid synthase subunit alpha (EC 2.3.1.86) (p190/210) [I: Acyl carrier; 3-oxoacyl-{acyl-carrier protein} reductase (EC 1.1.1.100) (Beta-ketoacyl reductase); 3-oxoacyl-{acyl-car} protein] synthase (EC 2.3.1.41) (Beta-ketoacyl synthase)].
FAS2 OR LSD1 OR SPAC4A8.11C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales; Schizosaccharomycetales; Schizosaccharomyces.
NCBI_TaxID=4896;
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PROSITE; PS00502; POLYGALACTUR
Hydrolase; Glycosidase; Cell w
SIGNAL 1 20 F
CHAIN 21 376 F
SEQUENCE 376 AA; 38068 MW;
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SEQUENCE FROM N.A.
MEDLINE=96354912; Publy
Takahashi I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=972;
MEDLINE=21848401; P
Wood V., Gwilliam R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saitoh S., Takahashi K., Nabeshima K Hirata A., Yanagida M.; "Aberrant mitosis in fission yeast m synthetase and acetyl CoA carboxylas. J. Cell Biol. 134:949-961(1996).
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Cerrutti L., Lowe
Shpakovski G.V., I
"The genome seque!
Nature 415:871-88!
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J. Biol. Chem. 269:14103-14110(1994).

-!- FUNCTION: Fatty acid synthetase catalyzes the formation of long-chain fatty acids from acetyl-CoA, malonyl-CoA and NADPH. The alpha subunit contains domains for: acyl carrier protein, 3-oxoacyl-[acyl-carrier protein] reductase, and 3-oxoacyl-[acyl-carrier-protein] synthase. This subunit coordinates the binding of the six beta subunits to the enzyme complex.

-!- CATALYTIC ACTIVITY: Acetyl-CoA + N malonyl-CoA + 2N NADPH = a long-chain acyl-CoA + N CO(2) + 2N NADP(+).

-!- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + malonyl-[acyl-carrier protein] = 3-oxoacyl-[acyl-carrier protein] + CO(2) +
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"Schizosaccharomyces pombe fatty acid synthase mediates DNA strand
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MEDLINE=94245730;
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Cruzado L., Jimenez J., Sanchez M., del Rey F., Ben
A., Revuelta J.L., Moreno S., Armstrong J., Forsburg
., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
G.V., Ussery D., Barrell B.G., Nurse P.;
sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-215 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        ROT entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation - Bioinformatics Institute. There are no restrictions on its profit institutions as long as its content is in no way this statement is not removed. Usage by and for commercial lires a license agreement (See http://www.isb-sib.ch/announce/
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                                               ACYL CARRIER (ACP).
BETA-KETOACYL REDUCTASE.
BETA-KETOACYL SYNTHASE.
PHOSPHOPANTETHEINE (BY SIMILARITY).
BETA-KETOACYL SYNTHASE (BY SIMILARITY)
S -> A (IN REF. 4).
K -> R (IN REF. 1).
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l Rey F., Benito J.
J., Forsburg S.L.,
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Mammalia; Eutheria; (
Bovidae; Caprinae; Ovidae; [1]
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III) (NOSIII)
(Fragment).
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TISSUE=Endothelial cells;

Aguan K., Weiner C.P.;

"Effect of hypoxia on the microvasculature of developing fetal brain of sheep: a studies on the expression pattern of constitutive forms of nitric oxide synthase.";

Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Produces nitric oxide (NO) which is implicated in vascular smooth muscle relaxation through a cGMP-mediated signal transduction pathway. No mediates vascular endothelial growth factor (VEGF)-induced angiogenesis in coronary vessels and promotes blood clotting through the activation of platelets (By
                                                                                                                                                                                                 EMBL; U76738; AAB40705.1; -.
HSSP; P29473; 1D0C.
InterPro; IPR004030; NO_synthase
Pfam; PF02898; NO_synthase; 1.
PROSITE; PS60001; NOS; PARTIAL.
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X MEDLINE=96337999; PubMed=8688087;

A Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

A Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

A Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

A Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

A Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

A Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

A Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

A Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus

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Science 273:1058-1073(1996).
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Hypothetical
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PIR; D64316; D
TIGR; MJ0132;
InterPro; IPR0
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Methanocaldococcaceae; Methanocaldococcus.
NCBI_TaxID=2190;
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Pfam; PF02384; N6_Mtase; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 220 AA; 25766 MW; 710DDAE4C7A47954 CRC64;
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sequence
17, Appl
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SEQUENT 1. Application US/09632570 Sequence 17, Application US/09632570 Sequence 17, Application US/09632570 Sequence 17, Application US/09632570 Sequence 17, Application US/09632570 APPLICANT: Gualiteti, Peter Applicant: Phillips, Jay, Iay, Inc. Sequence 17 MILE OF INVENTION: Compositions FILE REFERENCE: GC631 CURRENT FAPLICATION NUMBER: US/09/632,570 CURRENT FAPLICATION NUMBER: US/09/632,575 DEAD IN 0. 1 SEQ ID NO 1. 1 CORGANISM: Glicalidium roseum (3) SEQ ID NO 1. 2 1 ADMSWA 6 1 ADMSWA 6 1 ADMSWA 6 1 ADMSWA 6 1 APPLICANT: Mitchinson, Colin APPLICANT: Mobaliteti, Peter APPLICANT: Mobalite Edili Compositions and Methods for Obtaining Same FILE REFERENCE: GC629 CURRENT APPLICATION NUMBER: US/09/632,575 CURRENT FILE OF INVENTION: Such Edili Compositions and Methods for Obtaining Same FILE REFERENCE: GC629 CURRENT FILE OF INVENTION: Such Edili Compositions and Methods for Obtaining Same FILE OF INVENTION: Such Edili Compositions and Methods for Obtaining Same FILE REFERENCE: GC629 CURRENT APPLICATION NUMBER: US/09/632,575 LENGTH: 236 SOFTWARE: Past-SQ for Windows Version 4.0 SSO ID NO 47 LENGTH: 236 LE	3 US-09-146-770-4 3 US-09-216-295-3 3 US-09-216-295-4 4 US-09-633-084-3 4 US-09-633-084-4 4 US-10-075-872-3 4 US-10-261-997-3 4 US-10-261-997-4 4 US-09-632-570-3 5 Equence 4, App Sequence 3, App Sequence 3, App Sequence 3, App Sequence 4, App Sequence 3, App Sequence 4, App Sequence 5, App Sequence 5, App Sequence 5, App Sequence 5,	8 33 82.5 232 4 US-10-075-872-1 Sequence 1, Appl 9 33 82.5 232 4 US-10-261-997-1 Sequence 1, Appl 0 :: 33 82.5 234 1 US-08-032-848C-9 Sequence 9, Appl 1 33 82.5 234 1 US-08-438-870-9 Sequence 9, Appl 2 33 82.5 234 1 US-08-146-770-3 Sequence 3 Appl 2
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RESULT 3
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LENGTH: 68
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APPLICANT: Marc J.
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APPLICANT: Marc J.
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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Patent No. 6451604;
GENERAL INFORMATION:
APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annett
           APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affect
TITLE OF INVENTION: death and their use
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,93
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
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LENGTH: 142
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                                                                                                                       Sequence 162, Application US/09325932A Patent No. 6451604 GENERAL INFORMATION:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Eucalyptus (
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TITLE OF INVENTION: Compositions affecting
TITLE OF INVENTION: death and their use in
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 SOFTWARE:
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GENERAL INFORMATION:

APPLICANT: Flinn, Barry

APPLICANT: Lasham, Annette

TITLE OF INVENTION: Compositions affecting p

TITLE OF INVENTION: death and their use in t

FILE REFERENCE: 1022

CURRENT APPLICATION NUMBER: US/09/325,932A

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 206

SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-345-236B-3
; Sequence 3, Ap
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; TYPE: PRT
; ORGANISM: Eucalyptus
US-09-325-932A-162
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APPLICANT: Cockburn, Andrew;
APPLICANT: White, Susan E.
APPLICANT: Undeen, Albert H.
TITLE OF INVENTION: No. 6521454el Baculoviruses, Institute Of INVENTION: Compositions, and Methods for Column Reference: 21042.0004;
CURRENT APPLICATION NUMBER: US/09/345,236B;
CURRENT FILING DATE: 1999-06-30;
NUMBER OF SEQ ID NOS: 148;
SOFTWARE: FastSEQ for Windows Version 3.0
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SOFTWARE: FastSEQ for
SEQ ID NO 3
LENGTH: 242
TYPE: PRT
ORGANISM: mosquito k
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Best Local S
Matches 5
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Matches 5
                                                                           SOFTWARE: FastSEQ for
SEQ ID NO 158
LENGTH: 378
TYPE: PRT
ORGANISM: Eucalyptus 93-09-325-932A-158
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uence 158, Appli
ent No. 6451604
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RESULT 12
US-08-905-223-274
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; ORGANISM: Pseudon
US-09-252-991A-21704
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US-09-252-991A-21
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SE(
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22368
LENGTH: 445
; Sequence 274, Application
; Patent No. 6222029
; GENERAL INFORMATION:
; APPLICANT: Edwards, i
; APPLICANT: Duelert, !
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21704
LENGTH: 467
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SEQ ID NO 2
LENGTH: 4
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GENERAL INFORMATION:
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RESULT 13
US-08-379-538-2
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SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEPAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 274:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 Amino acids
                                                                                                                                                                                                           Sequence
Patent No
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Best Loc
Matches
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                                                                                                                                                                                      GENERAL INFO
                    NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pfizer Inc
STREET: 235 East 42nd
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 44 amino a
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTE
ORIGINAL SOURCE:
                                                                                                           APPLICANT: Heck, St. APPLICANT: Ronau, ROTITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 92101-3505
COMPUTER READABLE FO
MEDIUM TYPE: Flo-
COMPUTER: IBM PC
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CORRESPONDENCE ADDRE
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LOCATION: -26..-1
IDENTIFICATION METHOD:
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                                                                                                                                                                                                              2, Application US/08379538
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READABLE
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Nason II, Deane
Heck, Steven D.
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PE: Floppy Disk
IBM PC compatible
SYSTEM: Win95
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FORM:
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score 9.6
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US-08-774-065-
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                                                                                                                                                                                                                                                                                                                                                       Sequence
Patent No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 34,462
REFERENCE/DOCKET NUMBER: PC81
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 573-4585
TELEFAX: (212) 573-1939
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Best I
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ORIGINAL SOURCE:
ORGANISM: Fili
TISSUE TYPE: V
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MOLECULE TYPE:
HYPOTHETICAL:
             APPLICATION FILING DATE PRIOR APPLICA
                                                                                                                                                                                                                                             TITLE OF
                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US93/03921
FILING DATE: 30-APRIL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Zielinski, Bryan
REGISTRATION NUMBER: 34,462
REFERENCE/DOCKET NUMBER: PC8175A
                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                        NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENENCOR INTERNATIONAL
STREET: 925 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 1
FILING DATE: 3-MAY-1:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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                                                                                                                                                               ADDRESSEE:
STREET: 92
CITY: PALC
STATE: CAL
                                                                                                                                      COUNTRY: U
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T: Larenas, Edmund
T: Ward, Michael
INVENTION: NOVEL OF
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CALIFORNIA
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CATION DATA:
ON NUMBER:
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Conservative
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
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Pred. No. 1.1e+02;
L; Mismatches 0;
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SECTITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23817
LENGTH: 164
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Glaister, Debra J.

REGISTRATION NUMBER: 33,888

REFERENCE/DOCKET NUMBER: GC368

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-846-7620

TELEFAX: 415-845-6504

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 136 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-774-065-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-09-252-991A-23817
; Sequence 23817, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
Search completed: April 26, Job time : 24 secs
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62 ADWQWS 67
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Similarity 66.7%;
4; Conservative
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5; Conservative
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Pred. No. 2e+02;
1; Mismatches
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1: /cgn2_6/ptodata/2/paa/US06_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US06_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US08_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US08_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US083_COMB.pep:*

9: /cgn2_6/ptodata/2/paa/US083_COMB.pep:*

10: /cgn2_6/ptodata/2/paa/US083_COMB.pep:*

11: /cgn2_6/ptodata/2/paa/US085_COMB.pep:*

12: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*

13: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*

14: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*

15: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*

16: /cgn2_6/ptodata/2/paa/US089_COMB.pep:*

17: /cgn2_6/ptodata/2/paa/US099_COMB.pep:*

18: /cgn2_6/ptodata/2/paa/US099_COMB.pep:*

19: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*

20: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*

21: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*

22: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*

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32: /cgn2_6/ptodata/2/paa/US00_COMB.pep:*

33: /cgn2_6/ptodata/2/paa/US00_COMB.pep:*

33: /cgn2_6/ptodata/2/paa/US00_COMB.pep:*

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ALIGNMENTS	9-643-260- 9-643-260- 9-847-940B 9-847-940B 9-847-946A	-10-072-851-509 -10-282-122A-43 -60-253-625-272 -60-257-931-355 -60-269-308-457 -10-366-683-238 -10-419-128-238	-60-143-992-1 -09-614-150A- -09-614-150A- -09-791-537-3 -60-173-464-1 -60-191-637-1 -60-191-681-1	US00-33878-47 09-147-729-16 09-284-327-22 09-284-327A-22 09-470-832-47 10-441-625-17 10-441-626-17 10-441-626-17	-09-643-26009-847-946A -09-847-946A
	equence 4, equence 5, equence 5, equence 5, equence 5,	equence 5090, A equence 43572, equence 2729, A equence 3557, A equence 4579, A equence 4579, A equence 23882, equence 23882,	equence 1469 equence 1469 equence 3263 equence 3263 equence 1202 equence 1473 equence 1161 quence 5090,	47, Appl 16, App 22, App 22, App 22, App 247, App 26 17, App 26 17, App 26 17, App 26 17, App 26 1376, A	equence 6, equence 73, equence 77, equence 78, equence 78, equence 78, equence 72, equence 75, equence 76, equence 71, equence 71, equence 71, equence 74, equence 74, equence 1549 equence 1549 equence 1549

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RESULT 1

US-09-643-260-6

IUS-09-643-260-6

IS Sequence 6, Application US/09643260

GENERAL INFORMATION:

APPLICANT: May, Michael J.

APPLICANT: Ghosh, Sankar;

TITLE OF INVENTION: Inhibition of NF-kappa B Activation by Blockade of IKK

TITLE OF INVENTION: beta-NEMO Interactions at the NEMO Binding Domain

FILE REFERENCE: 44574-5066-US

CURRENT APPLICATION NUMBER: US/09/643,260

CURRENT FILING DATE: 2000-08-22

PRIOR APPLICATION NUMBER: US 60/201,261

PRIOR APPLICATION NUMBER: US 60/201,261

PRIOR APPLICATION VET: 2.1

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 6

LENGTH: 6

TYPE: PRT

ORGANISM: Artificial Sequence

PEATURE:

OTHER INFORMATION: Description of Artificial Sequence: NBD mutant

OTHER INFORMATION: peptide sequence
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Result No.

Score

Query Match

Length

DB

IJ

Description

SUMMARIES

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APPLICANT: Hannig, Gerhard;
FILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USE
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 41
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                                                                                    APPLICANT: Hannig, Gerhard;
FILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: May, Mich
APPLICANT: Ghosh, S
APPLICANT: Findeis,
APPLICANT: Phillips
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SEQ ID NO 7
LENGTH: 6
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Best Local
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ORGANISM: Artificial S
FEATURE:
OTHER INFORMATION: Def
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                                     ORGANISM:
                                                   TYPE: PRT
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OTHER INFORMATION: OTHER INFORMATION:
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Phillips, Kathryn
Hannig, Gerhard
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5.5e+06;
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.5e+06;
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APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 70
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APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS ANI
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
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US-09-847-
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-847-946A-77
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Best Local S
Matches 6
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SEQ ID NO 77
LENGTH: 7
TYPE: PRT
ORGANISM:
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Description of Artificial Sequence: NEMO binding
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Pred. No. 5.5e+06;
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Pred. No. 5.5e+06;
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OTHER INFORMATION:

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RESULT 7
US-09-847-946A-69
; Sequence 69, Applicat
; GENERAL INFORMATION:
; APPLICANT: May, Mich
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US-09-847-946A-7
                                                               APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
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; OTHER INFORMATION:
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US-09-847-946A-78
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TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUN
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
COUNTY DE PALENTIN VEY: 2.0
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SEQ ID NO 7
LENGTH: 8
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GENERAL INFORMATION:
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ORGANISM: FEATURE:
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Phillips, Kathryn
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Phillips, Marthyn
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s, Mark A
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5.5e+06;
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RESULT
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OTHER INFORMATION:
US-09-847-946A-69
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                                                                                                                                                                                                                                                                                            RESULT
                                                                       APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AN
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
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Best Local S
Matches 6
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SEQ ID NO 7
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Best Local
SEQ ID NO 75
LENGTH: 9
TYPE: PRT
ORGANISM:
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OTHER INFORMATION:
09-847-946A-72
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CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: |09/643,260
PRIOR FILING DATE: 2000-08-22
                                                 SOFTWARE:
                                                                NUMBER
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TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND
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Ghosh,
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Findeis, Mark A
Phillips, Kathryn
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Pred. No. 5.5e+06;
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Pred. No.
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; FEATURE:
; OTHER INFORMAT
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US-09-847-946A-75
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US-09-847-946A-71
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APPLICANT: Findeis, Mark A

APPLICANT: Phillips, Kathryn

APPLICANT: Hannig, Gerhard

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND

FILE REFERENCE: PPI-119

CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: 60/201,261

PRIOR FILING DATE: 2000-05-02

PRIOR APPLICATION NUMBER: 09/643,260

PRIOR FILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 160

SOFTWARE: PatentIn Ver. 2.0
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SOFTWARE: Pater
SEQ ID NO 76
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Best Local S
Matches 6
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Best Local
Matches
                                                                                                                                                                                                                         Sequence 71, Application US/09847946A GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
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APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS
FILE REFERENCE: PPI-119
CURRENT ADDITION: ANTI-INFLAMMATORY COMPOUNDS
                                                                   PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
                                         SOFTWARE:
                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/847, CURRENT FILING DATE: 2001-05-02
                                                          NUMBER OF SEQ
                             EQ ID NO
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TYPE: PI
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RESULT 12
US-09-847-946A-7
; Sequence 74, A
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APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THE
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
                                    APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COPELLE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,940
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: May, Michael J

APPLICANT: Ghosh, Sankar

APPLICANT: Findeis, Mark A

APPLICANT: Phillips V--
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; OTHER INFORMATION:
US-09-847-946A-71
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SEQ ID NO 74
LENGTH: 10
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ORGANISM: Art
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Ghosh, Sankar
Findeis, Mark A
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Application US/09847946A
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US-09-284-327A-45

US-09-284-327A-45

Sequence 45, Application US/09284327A

GENERAL INFORMATION:

APPLICANT: Bower, Benjamin S.

APPLICANT: Fowler, Timothy

APPLICANT: Phillips, Jay I.

TITLE OF INVENTION: Novel EGIII-Like Enzymes, DN:

TITLE OF INVENTION: Such Enzymes and Methods fo:

FILE REFERENCE: GC516-2-US

CURRENT APPLICATION NUMBER: US/09/284,327A

CURRENT FILING DATE: 1999-04-10

PRIOR APPLICATION NUMBER: PCT/US98/26552

PRIOR APPLICATION NUMBER: PCT/US98/26552

PRIOR FILING DATE: 1998-12-14

NUMBER OF SEQ ID NOS: 68

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 45

LENGTH: 103

TYPE: PRT

ORGANISM: Gliocladium roseum

US-09-284-327A-45
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PCT-US01-01321-1549
; Sequence 1549, Application PC/TUS01013; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Nucleic Acids, P1; FILE REFERENCE: PC011PCT; CURRENT APPLICATION NUMBER: PCT/US01, CURRENT FILING DATE: 2001-01-17; NUMBER OF SEQ ID NOS: 2181; SOFTWARE: PatentIn Ver. 2.0; SEQ ID NO 1549; LENGTH: 33
; TYPE: PRT; ORGANISM: Homo sapiens; FEATURE:
; NAME/KEY: SITE; LOCATION: (3); OTHER INFORMATION: Xaa equals any of PCT-US01-01321-1549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Artificial S
; FEATURE:
; OTHER INFORMATION: Des
; OTHER INFORMATION: seq
US-09-847-946A-68
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Matches 5
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                         Score 37; DB 16;
Pred. No. 1.5e+03;
1; Mismatches 0;
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Producing
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Search completed: April 26, 2004, 13:13:10 Job time : 182 secs

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